β U #11

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Revised 01/29/2002

PCT09

RAW SEQUENCE LISTING   DATE: 12/04/2002
PATENT APPLICATION: **US/09/856,617A**   TIME: 13:50:11

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Output Set: **N:\CRF4\12032002\I856617A.raw**

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  5 <120> TITLE OF INVENTION: NOVEL POLYPEPTIDE
  7 <130> FILE REFERENCE: 766.52
  9 <140> CURRENT APPLICATION NUMBER: US 09/856,617A
 10 <141> CURRENT FILING DATE: 2001-05-24
 12 <150> PRIOR APPLICATION NUMBER: H10-332484
 13 <151> PRIOR FILING DATE: 1998-11-24
 15 <150> PRIOR APPLICATION NUMBER: H11-248442
 16 <151> PRIOR FILING DATE: 1999-09-02
 18 <160> NUMBER OF SEQ ID NOS: 18
 19 <170> SOFTWARE: PatentIn Ver. 2.0
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ERRORED SEQUENCES

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393 Cys Ser Gly Ser Val Met Ser Glu Arg Val Ser Gly Leu Ala Gly Ser
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396 atc tac cgc gag ttc gag cgc ctc att cac tgc tat gac gag gag gtg   259
397 Ile Tyr Arg Glu Phe Glu Arg Leu Ile His Cys Tyr Asp Glu Glu Val
398                  40                  45                  50
400 gtc aag gag ctc atg ccg ctg gtg gtg aac gtg ctg gag aac ctt gac   307
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402              55                  60                  65
404 tcg gtg ctg agc gag aac cag gag cac gag gtg gag ctg gag ctc cta   355
405 Ser Val Leu Ser Glu Asn Gln Glu His Glu Val Glu Leu Glu Leu Leu
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408 cgc gag gac aac gag cag ctg ctc acg caa tac gag cgc gag aag gcg   403
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676 cat cga ggc cag ctc cta ggg ctc cga gcc aac aag aca tcc cca aca   3619
677 His Arg Gly Gln Leu Leu Gly Leu Arg Ala Asn Lys Thr Ser Pro Thr
678              1160                1165                1170
680 tct ggg gag ggg acc cgc cca ggg ggc atc atc cat gtg tat ggg gac   3667
681 Ser Gly Glu Gly Thr Arg Pro Gly Gly Ile Ile His Val Tyr Gly Asp
682         1175              1180                1185
684 gac agc agt gac aag gcc gcc agt agt ttc atc ccc tac tgc tcc atg   3715
685 Asp Ser Ser Asp Lys Ala Ala Ser Ser Phe Ile Pro Tyr Cys Ser Met
686        1190              1195                1200
688 gca cag gct cag ctt tgc ttc cat ggg cac cgt gat gct gtc aaa ttc   3763
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692 ttt gtc tct gtg cca gga aat gtg ctg gcc act ctc aat ggc agt gtg   3811
693 Phe Val Ser Val Pro Gly Asn Val Leu Ala Thr Leu Asn Gly Ser Val
694 1220             1225                1230                1235
696 cta gac agc cca tca gag ggc cct ggg cct gct gca ccc gct gca gat   3859
697 Leu Asp Ser Pro Ser Glu Gly Pro Gly Pro Ala Ala Pro Ala Ala Asp
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700 gct gag ggc cag aag ttg aag aat gca ctg gtg ctg agt ggt ggt gaa   3907
701 Ala Glu Gly Gln Lys Leu Lys Asn Ala Leu Val Leu Ser Gly Gly Glu
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704 ggt tac att gac ttc cgt atc gga gac gga gag gat gat gaa act gag   3955
705 Gly Tyr Ile Asp Phe Arg Ile Gly Asp Gly Glu Asp Asp Glu Thr Glu
706        1270              1275                1280
708 gaa tgt gcc ggg gac gtg aac cag aca aag ccc tcg ttg tcc aag gct   4003
709 Glu Cys Ala Gly Asp Val Asn Gln Thr Lys Pro Ser Leu Ser Lys Ala
710    1285              1290                1295
E--> 712 gag cgc agc cac atc atc gtg tgg cag gtg tcc tac acc cct gag   4043
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714 1300             1305                1310
E--> 716 tgagaccctg tcctacctga tgccaactgt acataggacc ctacctgcct gcctccccgc 4102
E--> 718 ctgttccctg gggcagccag gttcgtccat ccccttttaa cctctcaact tgcagctttt 4162
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(4043) — Counted 4045

Seq. 8

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2121 gag tct gat ggt gag gat gag cat gag gca ggc cgt gcc ggg cag cca    963
2122 Glu Ser Asp Gly Glu Asp Glu His Glu Ala Gly Arg Ala Gly Gln Pro
2123      305              310              315
2125 gag gct ggt gat ggg acc acc gag atc tca ccc act ggt gct gct ggt    1011
2126 Glu Ala Gly Asp Gly Thr Thr Glu Ile Ser Pro Thr Gly Ala Ala Gly
2127 320              325              330              335
2129 cct gag aag agg atg gag aag aag acg gag cag cag cgg cgg cgg gag    1059
2130 Pro Glu Lys Arg Met Glu Lys Lys Thr Glu Gln Gln Arg Arg Arg Glu
2131            340              345              350
2133 aaa gct gct cgc aag ctg cgg gtg cag cag gct gca ctg agg gca gcc    1107
2134 Lys Ala Ala Arg Lys Leu Arg Val Gln Gln Ala Ala Leu Arg Ala Ala
2135         355              360              365
2137 cgg ctt cag cac caa gaa ctt ttc agg ctg cgt ggg atc aag gcc cag    1155
2138 Arg Leu Gln His Gln Glu Leu Phe Arg Leu Arg Gly Ile Lys Ala Gln
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2141 gtg gcc cga agg ctg gca gaa ctg gca cgc cgg agg gag cag cgg cgc    1203
2142 Val Ala Arg Arg Leu Ala Glu Leu Ala Arg Arg Arg Glu Gln Arg Arg
2143      385              390              395
2145 ata cgg cga ctg gca gag gct gac aag ccc cga agg ctg gga cgg ctc    1251
2146 Ile Arg Arg Leu Ala Glu Ala Asp Lys Pro Arg Arg Leu Gly Arg Leu
2147 400              405              410              415
2149 aag tac cag gct cct gac att gat gtg cag ctc agc tct gag ttg tct    1299
2150 Lys Tyr Gln Ala Pro Asp Ile Asp Val Gln Leu Ser Ser Glu Leu Ser
2151            420              425              430
2153 ggc tca ctc agg aca ctg aag cca gaa ggt cac att ctc cga gac agg    1347
2154 Gly Ser Leu Arg Thr Leu Lys Pro Glu Gly His Ile Leu Arg Asp Arg
2155         435              440              445
2157 ttc aag agc ttc cag aag aga aat atg att gag ccc cga gaa cga gcc    1395
2158 Phe Lys Ser Phe Gln Lys Arg Asn Met Ile Glu Pro Arg Glu Arg Ala
2159         450              455              460
2161 aag ttc aag cgc aaa tac aaa gtg aag ctg gtg gag aag cgg gcc tac    1443
2162 Lys Phe Lys Arg Lys Tyr Lys Val Lys Leu Val Glu Lys Arg Ala Tyr
2163      465              470              475
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     2173 <213> ORGANISM: Mouse
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RAW SEQUENCE LISTING   DATE: 12/04/2002
PATENT APPLICATION: **US/09/856,617A**   TIME: 13:50:11

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2333         835             840             845
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2338 Thr Glu Ala Thr Glu Val Pro Asp Pro Gly Pro Ser Glu Ser Glu Ala
2339 865             870             875             880
2341 Thr Thr Val Arg Pro Gly Pro Leu Thr Glu His Val Phe Thr Asp Pro
2342         885             890             895
2344 Ala Pro Thr Pro Ser Ser Ser Thr Gln Pro Ala Ser Glu Asn Gly Ser
2345         900             905             910
2347 Glu Ser Asn Gly Thr Ile Val Gln Pro Gln Val Glu Pro Ser Gly Glu
2348         915             920             925
2350 Leu Ser Thr Thr Thr Ser Ser Ala Ala Pro Thr Met Trp Leu Gly Ala
2351         930             935             940
2353 Gln Asn Gly Trp Leu Tyr Val His Ser Ala Val Ala Asn Trp Lys Lys
2354 945             950             955             960
2356 Cys Leu His Ser Ile Lys Leu Lys Asp Ser Val Leu Ser Leu Val His
2357         965             970             975
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2360         980             985             990
2362 Phe His Arg Gly Glu Asp Gly Gln Trp Asp Leu Ser Asn Tyr His Leu
2363         995             1000            1005
2365 Met Asp Leu Gly His Pro His His Ser Ile Arg Cys Met Ala Val Val
2366     1010            1015            1020
2368 Asn Asp Arg Val Trp Cys Gly Tyr Lys Asn Lys Val His Val Ile Gln
2369 1025            1030            1035            1040
2371 Pro Lys Thr Met Gln Ile Glu Lys Ser Phe Asp Ala His Pro Arg Arg
2372         1045            1050            1055
2374 Glu Ser Gln Val Arg Gln Leu Ala Trp Ile Gly Asp Gly Val Trp Val
2375         1060            1065            1070
2377 Ser Ile Arg Leu Asp Ser Thr Leu Arg Leu Tyr His Ala His Thr His
2378         1075            1080            1085
2380 Gln His Leu Gln Asp Val Asp Ile Glu Pro Tyr Val Ser Lys Met Leu
2381     1090            1095            1100
2383 Gly Thr Gly Lys Leu Gly Phe Ser Phe Val Arg Ile Thr Ala Leu Leu
2384 1105            1110            1115            1120
2386 Ile Ala Gly Asn Arg Leu Trp Val Gly Thr Gly Asn Gly Val Val Ile
2387         1125            1130            1135
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2390         1140            1145            1150
2392 Gly Leu Arg Ala Asn Lys Thr Ser Pro Thr Ser Gly Glu Gly Thr Arg
2393         1155            1160            1165
2395 Pro Gly Gly Ile Ile His Val Tyr Gly Asp Asp Ser Ser Asp Lys Ala
2396     1170            1175            1180
2398 Ala Ser Ser Phe Ile Pro Tyr Cys Ser Met Ala Gln Ala Gln Leu Cys
2399 1185            1190            1195            1200
2401 Phe His Gly His Arg Asp Ala Val Lys Phe Phe Val Ser Val Pro Gly
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E--> 2369|025
E--> 2384 |105
E--> 2399 |185

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2402              1205              1210              1215
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2407 Gly Pro Gly Pro Ala Ala Pro Ala Ala Asp Ala Glu Gly Gln Lys Leu
2408      1235              1240              1245
2410 Lys Asn Ala Leu Val Leu Ser Gly Gly Glu Gly Tyr Ile Asp Phe Arg
2411    1250              1255              1260
2413 Ile Gly Asp Gly Glu Asp Asp Glu Thr Glu Glu Cys Ala Gly Asp Val
E--> 2414 1265              1270              1275              1280
2416 Asn Gln Thr Lys Pro Ser Leu Ser Lys Ala Glu Arg Ser His Ile Ile
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2426 <213> ORGANISM: Mouse
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2435 Ala Gly Ser Ile Tyr Arg Glu Phe Glu Arg Leu Ile His Cys Tyr Asp
2436         35              40              45
2438 Glu Glu Val Val Lys Glu Leu Met Pro Leu Val Val Asn Val Leu Glu
2439      50              55              60
2441 Asn Leu Asp Ser Val Leu Ser Glu Asn Gln Glu His Glu Val Glu Leu
2442 65              70              75              80
2444 Glu Leu Leu Arg Glu Asp Asn Glu Gln Leu Leu Thr Gln Tyr Glu Arg
2445              85              90              95
2447 Glu Lys Ala Leu Arg Lys Gln Ala Glu Glu Lys Phe Ile Glu Phe Glu
2448           100             105             110
2450 Asp Ala Leu Glu Gln Glu Lys Lys Glu Leu Gln Ile Gln Val Glu His
2451         115             120             125
2453 Tyr Glu Phe Gln Thr Arg Gln Leu Glu Leu Lys Ala Lys Asn Tyr Ala
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2460           165             170             175
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2466      195             200             205
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2469      210             215             220
2471 Gly Met Cys Pro Asn Asp Glu Met Ser Glu Ser Gly Gln Ser Ser Ala
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RAW SEQUENCE LISTING   DATE: 12/04/2002
PATENT APPLICATION: **US/09/856,617A**   TIME: 13:50:11

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Output Set: **N:\CRF4\12032002\I856617A.raw**

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     2628              1060              1065              1070
     2630 Ala Trp Ile Gly Asp Gly Val Trp Val Ser Ile Arg Leu Asp Ser Thr
     2631         1075              1080              1085
     2633 Leu Arg Leu Tyr His Ala His Thr His Gln His Leu Gln Asp Val Asp
     2634      1090              1095              1100
     2636 Ile Glu Pro Tyr Val Ser Lys Met Leu Gly Thr Gly Lys Leu Gly Phe
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     2640              1125              1130              1135
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     2643         1140              1145              1150
     2645 Val Val Leu His Arg Gly Gln Leu Leu Gly Leu Arg Ala Asn Lys Thr
     2646         1155              1160              1165
     2648 Ser Pro Thr Ser Gly Glu Gly Thr Arg Pro Gly Gly Ile Ile His Val
     2649      1170              1175              1180
     2651 Tyr Gly Asp Asp Ser Ser Asp Lys Ala Ala Ser Ser Phe Ile Pro Tyr
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     2658         1220              1225              1230
     2660 Gly Ser Val Leu Asp Ser Pro Ser Glu Gly Pro Gly Pro Ala Ala Pro
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     2664      1250              1255              1260
     2666 Gly Gly Glu Gly Tyr Ile Asp Phe Arg Ile Gly Asp Gly Glu Asp Asp
E--> 2667 |265              1270              1275              1280
     2669 Glu Thr Glu Glu Cys Ala Gly Asp Val Asn Gln Thr Lys Pro Ser Leu
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     2689              20              25              30
     2691 Ala Gly Ser Ile Tyr Arg Glu Phe Glu Arg Leu Ile His Cys Tyr Asp
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Seq. 11

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2850 Thr Thr Ala Asn Gly Lys Val Asn Pro Ser Gln Ser Thr Glu Glu Ala
2851                 885                 890                 895
2853 Thr Glu Ala Thr Glu Val Pro Asp Pro Gly Pro Ser Glu Ser Glu Ala
2854                 900                 905                 910
2856 Thr Thr Val Arg Pro Gly Pro Leu Thr Glu His Val Phe Thr Asp Pro
2857             915                 920                 925
2859 Ala Pro Thr Pro Ser Ser Ser Thr Gln Pro Ala Ser Glu Asn Gly Ser
2860      930                 935                 940
2862 Glu Ser Asn Gly Thr Ile Val Gln Pro Gln Val Glu Pro Ser Gly Glu
2863 945                 950                 955                 960
2865 Leu Ser Thr Thr Thr Ser Ser Ala Ala Pro Thr Met Trp Leu Gly Ala
2866                 965                 970                 975
2868 Gln Asn Gly Trp Leu Tyr Val His Ser Ala Val Ala Asn Trp Lys Lys
2869                 980                 985                 990
2871 Cys Leu His Ser Ile Lys Leu Lys Asp Ser Val Leu Ser Leu Val His
2872             995                 1000                1005
2874 Val Lys Gly Arg Val Leu Val Ala Leu Ala Asp Gly Thr Leu Ala Ile
2875      1010                1015                ·1020
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2884             1060                1065                1070
2886 Pro Lys Thr Met Gln Ile Glu Lys Ser Phe Asp Ala His Pro Arg Arg
2887      1075                1080                1085
2889 Glu Ser Gln Val Arg Gln Leu Ala Trp Ile Gly Asp Gly Val Trp Val
2890 1090                1095                1100
2892 Ser Ile Arg Leu Asp Ser Thr Leu Arg Leu Tyr His Ala His Thr His
E--> 2893|105                1110                1115                1120
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2896                 1125                1130                1135
2898 Gly Thr Gly Lys Leu Gly Phe Ser Phe Val Arg Ile Thr Ala Leu Leu
2899                 1140                1145                1150
2901 Ile Ala Gly Asn Arg Leu Trp Val Gly Thr Gly Asn Gly Val Val Ile
2902      1155                1160                1165
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2916 Phe His Gly His Arg Asp Ala Val Lys Phe Phe Val Ser Val Pro Gly
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2920    1250               1255               1260
2922 Gly Pro Gly Pro Ala Ala Pro Ala Ala Asp Ala Glu Gly Gln Lys Leu
E--> 2923|265               1270               1275               1280
2925 Lys Asn Ala Leu Val Leu Ser Gly Gly Glu Gly Tyr Ile Asp Phe Arg
2926            1285               1290                1295
2928 Ile Gly Asp Gly Glu Asp Asp Glu Thr Glu Glu Cys Ala Gly Asp Val
2929            1300               1305                1310
2931 Asn Gln Thr Lys Pro Ser Leu Ser Lys Ala Glu Arg Ser His Ile Ile
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2954    50                55                60
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2960            85                90                95
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2963            100               105               110
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2968 Tyr Glu Phe Gln Thr Arg Gln Leu Glu Leu Lys Ala Lys Asn Tyr Ala
2969    130               135               140
2971 Asp Gln Ile Ser Arg Leu Glu Glu Arg Glu Ser Glu Met Lys Lys Glu
2972 145               150               155               160
2974 Tyr Asn Ala Leu His Gln Arg His Thr Glu Met Ile Gln Thr Tyr Val
2975            165               170               175
2977 Glu His Ile Glu Arg Ser Lys Met Gln Gln Val Gly Gly Ser Gly Gln
2978            180               185               190
2980 Thr Glu Ser Ser Leu Pro Gly Arg Arg Lys Glu Arg Pro Thr Ser Leu
2981            195               200               205
2983 Asn Val Phe Pro Leu Ala Asp Gly Met Val Arg Ala Gln Met Gly Gly
2984    210               215               220
2986 Lys Leu Val Pro Ala Gly Asp His Trp His Leu Ser Asp Leu Gly Gln
2987 225               230               235               240
2989 Leu Gln Ser Ser Ser Ser Tyr Gln Cys Pro Asn Asp Glu Met Ser Glu
```

```
E--> 3137|025            1030            1035            1040
     3139 Asp Leu Gly His Pro His His Ser Ile Arg Cys Met Ala Val Val Asn
     3140            1045            1050            1055
     3142 Asp Arg Val Trp Cys Gly Tyr Lys Asn Lys Val His Val Ile Gln Pro
     3143            1060            1065            1070
     3145 Lys Thr Met Gln Ile Glu Lys Ser Phe Asp Ala His Pro Arg Arg Glu
     3146       1075            1080            1085
     3148 Ser Gln Val Arg Gln Leu Ala Trp Ile Gly Asp Gly Val Trp Val Ser
     3149    1090            1095            1100
     3151 Ile Arg Leu Asp Ser Thr Leu Arg Leu Tyr His Ala His Thr His Gln
E--> 3152|105            1110            1115            1120
     3154 His Leu Gln Asp Val Asp Ile Glu Pro Tyr Val Ser Lys Met Leu Gly
     3155            1125            1130            1135
     3157 Thr Gly Lys Leu Gly Phe Ser Phe Val Arg Ile Thr Ala Leu Leu Ile
     3158            1140            1145            1150
     3160 Ala Gly Asn Arg Leu Trp Val Gly Thr Gly Asn Gly Val Val Ile Ser
     3161       1155            1160            1165
     3163 Ile Pro Leu Thr Glu Thr Val Val Leu His Arg Gly Gln Leu Leu Gly
     3164    1170            1175            1180
     3166 Leu Arg Ala Asn Lys Thr Ser Pro Thr Ser Gly Glu Gly Thr Arg Pro
E--> 3167|185            1190            1195            1200
     3169 Gly Gly Ile Ile His Val Tyr Gly Asp Asp Ser Ser Asp Lys Ala Ala
     3170            1205            1210            1215
     3172 Ser Ser Phe Ile Pro Tyr Cys Ser Met Ala Gln Ala Gln Leu Cys Phe
     3173            1220            1225            1230
     3175 His Gly His Arg Asp Ala Val Lys Phe Phe Val Ser Val Pro Gly Asn
     3176       1235            1240            1245
     3178 Val Leu Ala Thr Leu Asn Gly Ser Val Leu Asp Ser Pro Ser Glu Gly
     3179    1250            1255            1260
     3181 Pro Gly Pro Ala Ala Pro Ala Ala Asp Ala Glu Gly Gln Lys Leu Lys
E--> 3182|265            1270            1275            1280
     3184 Asn Ala Leu Val Leu Ser Gly Gly Glu Gly Tyr Ile Asp Phe Arg Ile
     3185            1285            1290            1295
     3187 Gly Asp Gly Glu Asp Asp Glu Thr Glu Glu Cys Ala Gly Asp Val Asn
     3188            1300            1305            1310
     3190 Gln Thr Lys Pro Ser Leu Ser Lys Ala Glu Arg Ser His Ile Ile Val
     3191       1315            1320            1325
     3193 Trp Gln Val Ser Tyr Thr Pro Glu
     3194    1330            1335
     3285 <210> SEQ ID NO: 14
     3286 <211> LENGTH: 1508
     3287 <212> TYPE: PRT
     3288 <213> ORGANISM: Mouse
     3290 <400> SEQUENCE: 14
     3291 Met Met Ala Gly Glu Gly Ser Thr Ile Thr Ser Arg Ile Lys Asn Leu
     3292    1         5                10               15
     3294 Leu Arg Ser Pro Ser Ile Lys Leu Arg Arg Ser Lys Ala Gly Asn Arg
     3295            20              25               30
     3297 Arg Glu Asp Leu Ser Ser Lys Val Thr Leu Glu Lys Val Leu Gly Val
```

See. 14

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3445               820              825              830
3447 Met Ser Arg Ala Gln Glu Thr Met Glu Tyr Leu Asp Pro Ala Pro Val
3448          835              840              845
3450 Ala Asn Thr Gly Pro Lys Arg Arg Gly Arg Trp Ala Gln Pro Gly Val
3451      850              855              860
3453 Glu Leu Ser Val Arg Ser Met Leu Asp Leu Arg Gln Ile Glu Thr Leu
3454 865              870              875              880
3456 Ala Pro Ser Pro Arg Gly Pro Ser Gln Asp Ser Leu Ala Val Ser Pro
3457              885              890              895
3459 Ala Gly Pro Gly Lys His Gly Pro Gln Ala Pro Glu Leu Ser Cys Val
3460              900              905              910
3462 Ser Gln Asn Glu Arg Ala Pro Arg Leu Gln Thr Ser Gln Pro Cys Ser
3463          915              920              925
3465 Cys Pro Asp Ile Ile Gln Leu Leu Ser Gln Glu Glu Gly Val Phe Ala
3466      930              935              940
3468 Gln Asp Leu Glu Pro Ala Pro Ile Glu Asp Gly Ile Val Tyr Pro Glu
3469 945              950              955              960
3471 Pro Ser Asp Ser Pro Thr Met Asp Thr Ser Ala Phe Gln Val Gln Ala
3472              965              970              975
3474 Pro Thr Gly Gly Ser Leu Gly Arg Met Tyr Pro Gly Ser Arg Gly Ser
3475          980              985              990
3477 Glu Lys His Ser Pro Asp Ser Ala Cys Ser Val Asp Tyr Ser Ser Ser
3478          995              1000             1005
3480 Arg Leu Ser Ser Pro Glu His Pro Asn Glu Asp Ser Glu Ser Thr Glu
3481      1010             1015             1020
3483 Pro Leu Ser Val Asp Gly Ile Ser Ser Asp Leu Glu Glu Pro Ala Glu
E--> 3484 |025             1030             1035             1040
3486 Gly Asp Glu Asp Glu Glu Glu Glu Gly Gly Thr Gly Leu Cys Gly Leu
3487              1045             1050             1055
3489 Gln Glu Gly Gly Pro Arg Thr Pro Asp Gln Glu Gln Phe Leu Lys Gln
3490          1060             1065             1070
3492 Leu Phe Glu Thr Leu Ala Asn Gly Thr Ala Pro Gly Gly Pro Ala Arg
3493      1075             1080             1085
3495 Val Leu Glu Arg Thr Glu Ser Arg Ser Ile Ser Ser Arg Phe Leu Leu
3496      1090             1095             1100
3498 Gln Val Gln Thr Leu Pro Leu Arg Glu Pro Ser Leu Ser Ser Ser Gly
E--> 3499 |105             1110             1115             1120
3501 Leu Ala Leu Thr Ser Arg Pro Asp Gln Val Ser Gln Val Ser Gly Glu
3502              1125             1130             1135
3504 Gln Leu Lys Gly Ser Gly Ala Thr Pro Pro Gly Ala Pro Pro Glu Met
3505          1140             1145             1150
3507 Glu Pro Ser Ser Gly Asn Ser Gly Pro Lys Gln Val Ala Pro Val Leu
3508          1155             1160             1165
3510 Leu Thr Arg Arg Arg Asn Asn Leu Asp Asn Ser Trp Ala Ser Lys Lys
3511      1170             1175             1180
3513 Met Ala Ala Thr Arg Pro Leu Ala Gly Leu Gln Lys Ala Gln Ser Val
E--> 3514 |185             1190             1195             1200
3516 His Ser Leu Val Pro Gln Asp Glu Val Pro Ser Ser Arg Pro Leu Leu
3517              1205             1210             1215
```

```
     3519 Phe Arg Glu Ala Glu Thr Gln Gly Ser Leu Gly Ser Leu Pro Gln Ala
     3520             1220             1225             1230
     3522 Gly Gly Cys Ser Ser Gln Pro His Ser Tyr Gln Asn His Thr Thr Ser
     3523         1235             1240             1245
     3525 Ser Met Ala Lys Leu Ala Arg Ser Ile Ser Val Gly Glu Asn Pro Gly
     3526     1250             1255             1260
     3528 Leu Ala Thr Glu Pro Gln Ala Pro Ala Pro Ile Arg Ile Ser Pro Phe
E--> 3529 |265            1270             1275             1280
     3531 Asn Lys Leu Ala Leu Pro Ser Arg Ala His Leu Val Leu Asp Ile Pro
     3532             1285             1290             1295
     3534 Lys Pro Leu Pro Asp Arg Pro Thr Leu Thr Thr Phe Ser Pro Val Ser
     3535         1300             1305             1310
     3537 Lys Gly Leu Thr His Asn Glu Thr Glu Gln Ser Gly Pro Leu Arg Glu
     3538         1315             1320             1325
     3540 Pro Arg Lys Ala His Thr Thr Val Glu Lys His Ser Cys Leu Gly Glu
     3541     1330             1335             1340
     3543 Gly Thr Thr His Lys Ser Arg Thr Glu Cys Gln Ala Tyr Pro Gly Pro
E--> 3544 |345            1350             1355             1360
     3546 Asn His Pro Cys Arg Gln Gln Leu Pro Val Asn Asn Leu Leu Gln Ala
     3547             1365             1370             1375
     3549 Glu Ser Leu Gln Pro Leu Ser Pro Glu Lys Thr Arg Asn Pro Val Glu
     3550         1380             1385             1390
     3552 Ser Ser Arg Pro Gly Val Ala Leu Ser Gln Asp Ser Glu Leu Ala Leu
     3553     1395             1400             1405
     3555 Ser Leu Gln Gln Cys Glu Gln Leu Val Ala Glu Leu Gln Gly Asn Val
     3556     1410             1415             1420
     3558 Arg Gln Ala Val Glu Leu Tyr Arg Ala Val Thr Ser Cys Lys Thr Pro
E--> 3559 |425            1430             1435             1440
     3561 Ser Ala Glu Gln Ser His Ile Thr Arg Leu Leu Arg Asp Thr Phe Ser
     3562             1445             1450             1455
     3564 Pro Val Arg Gln Glu Leu Glu Val Leu Ala Gly Ala Val Leu Ser Ser
     3565         1460             1465             1470
     3567 Pro Gly Gly Ser Pro Gly Ala Val Ala Ala Glu Gln Thr Gln Ala Leu
     3568     1475             1480             1485
     3570 Leu Glu Gln Tyr Ser Glu Leu Leu Leu Arg Ala Val Glu Arg Arg Met
     3571     1490             1495             1500
     3573 Glu Arg Arg Leu
E--> 3574 |505
     3730 <210> SEQ ID NO: 17
     3731 <211> LENGTH: 27
     3732 <212> TYPE: DNA
     3733 <213> ORGANISM: Artificial Sequence
     3735 <220> FEATURE:
     3736 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
     3738 <400> SEQUENCE: 17
E--> 3739 tagatatcgc cttggaacaa gagaaga
     3740 27
     3743 <210> SEQ ID NO: 18
     3744 <211> LENGTH: 31
```

(handwritten) → place here

```
3745 <212> TYPE: DNA
3746 <213> ORGANISM: Artificial Sequence
3748 <220> FEATURE:
3749 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
3751 <400> SEQUENCE: 18
3752 atgaattctc agttgttctt tgtgacactg a                              31
E--> 3753 1 / 142  delete
```

VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/856,617A**

DATE: 12/04/2002
TIME: 13:50:12

Input Set : **A:\SEQUENCE LISTING.txt**
Output Set: **N:\CRF4\12032002\I856617A.raw**

```
L:712  M:254 E: No. of Bases conflict, LENGTH:Input:4043 Counted:4048 SEQ:2
M:254 Repeated in SeqNo=2
L:2165 M:254 E: No. of Bases conflict, LENGTH:Input:1469 Counted:1472 SEQ:8
L:2167 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1469 Found:1472 SEQ:8
L:2369 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9
M:332 Repeated in SeqNo=9
L:2622 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
M:332 Repeated in SeqNo=10
L:2878 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:11
M:332 Repeated in SeqNo=11
L:3137 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:12
M:332 Repeated in SeqNo=12
L:3484 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:14
M:332 Repeated in SeqNo=14
L:3739 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:27 SEQ:17
L:3753 M:254 E: No. of Bases conflict, LENGTH:Input:142 Counted:32 SEQ:18
L:3753 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:3753 M:252 E: No. of Seq. differs, <211> LENGTH:Input:31 Found:32 SEQ:18
```